



wwPDB X-ray Structure Validation Summary Report ⓘ

May 21, 2020 – 07:53 pm BST

PDB ID : 2GNU
Title : The crystallization of reaction center from Rhodobacter sphaeroides occurs via a new route
Authors : Wadsten, P.; Woehri, A.B.; Snijder, A.; Katona, G.; Gardiner, A.T.; Cogdell, R.J.; Neutze, R.; Engstroem, S.
Deposited on : 2006-04-11
Resolution : 2.20 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

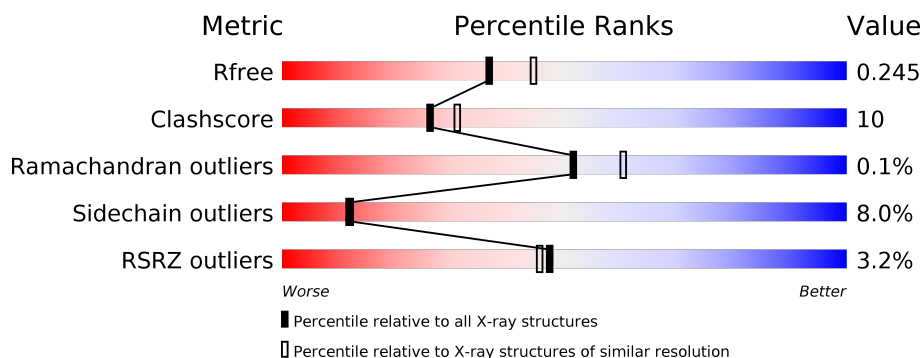
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	H	235	<div> <div>4%</div> <div> <div></div> <div>79%</div> <div>17%</div> <div>.</div> </div> </div>
2	L	281	<div> <div>4%</div> <div> <div></div> <div>78%</div> <div>18%</div> <div>.</div> </div> </div>
3	M	300	<div> <div>2%</div> <div> <div></div> <div>85%</div> <div>12%</div> <div>.</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	BCL	L	1282	X	-	-	-
5	BCL	L	1283	X	-	-	-
5	BCL	M	1303	X	-	-	-
9	BPH	M	1284	X	-	-	-
9	BPH	M	1304	X	-	-	-

2 Entry composition [i](#)

There are 11 unique types of molecules in this entry. The entry contains 7045 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Reaction center protein H chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	H	235	Total	C	N	O	S	0	0	0
			1787	1143	304	331	9			

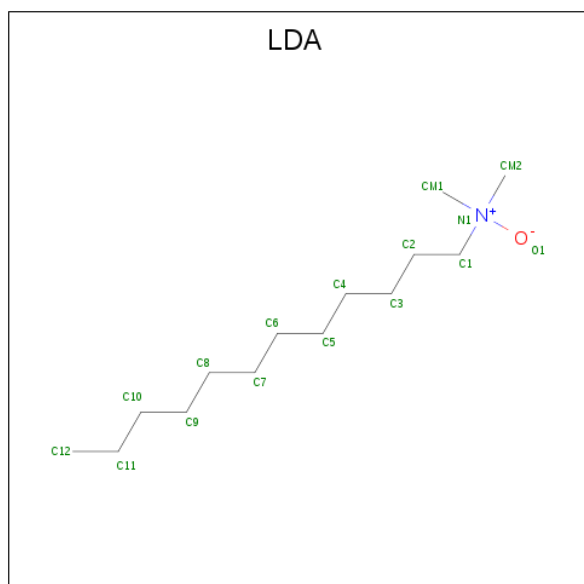
- Molecule 2 is a protein called Reaction center protein L chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	281	Total	C	N	O	S	0	0	0
			2232	1507	355	362	8			

- Molecule 3 is a protein called Reaction center protein M chain.

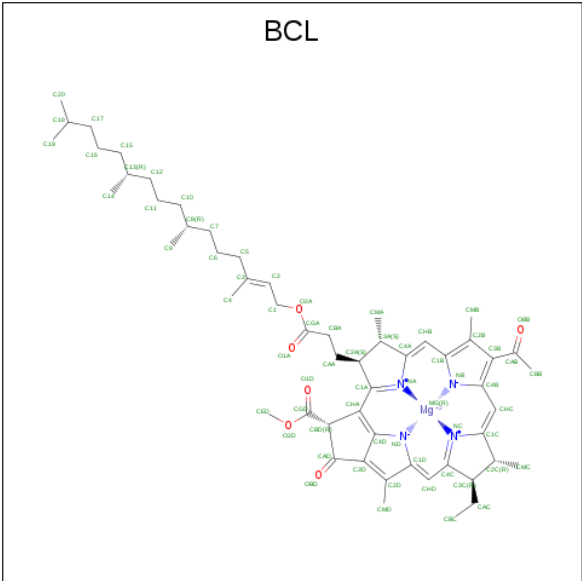
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	M	300	Total	C	N	O	S	0	0	0
			2400	1602	392	396	10			

- Molecule 4 is LAURYL DIMETHYLAMINE-N-OXIDE (three-letter code: LDA) (formula: $C_{14}H_{31}NO$).



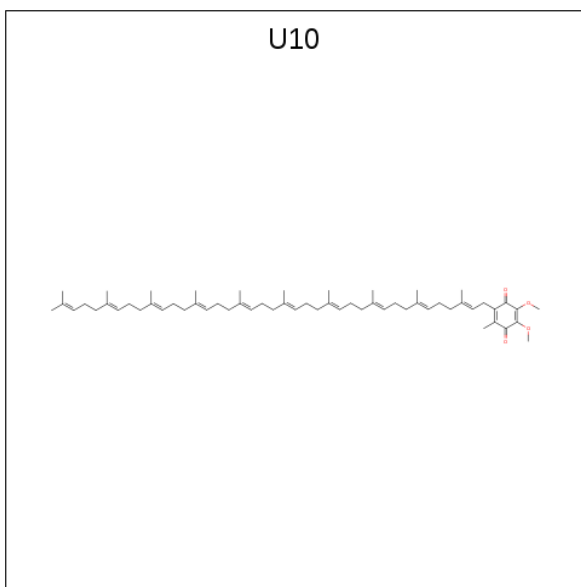
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	H	1	Total	C	N	O	0	0
			14	12	1	1		

- Molecule 5 is BACTERIOCHLOROPHYLL A (three-letter code: BCL) (formula: C₅₅H₇₄MgN₄O₆).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	L	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		
5	L	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		
5	M	1	Total	C	Mg	N	O	0	0
			48	37	1	4	6		
5	M	1	Total	C	Mg	N	O	0	0
			66	55	1	4	6		

- Molecule 6 is UBIQUINONE-10 (three-letter code: U10) (formula: C₅₉H₉₀O₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	L	1	Total	C	O	0	0
			24	20	4		
6	M	1	Total	C	O	0	0
			45	41	4		

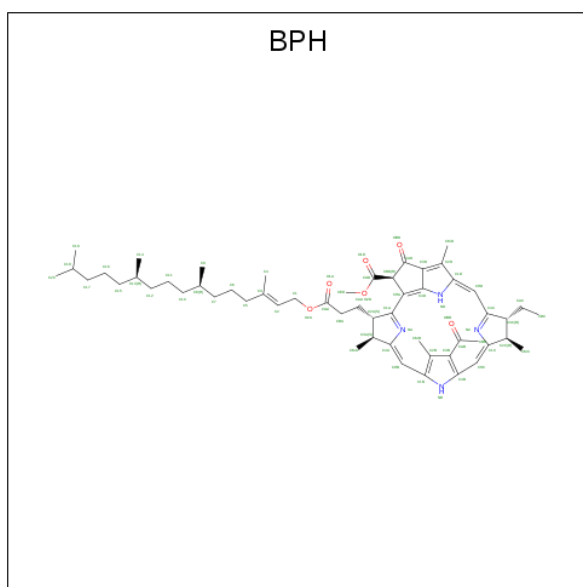
- Molecule 7 is FE (II) ION (three-letter code: FE2) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	M	1	Total	Fe	0	0
			1	1		

- Molecule 8 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

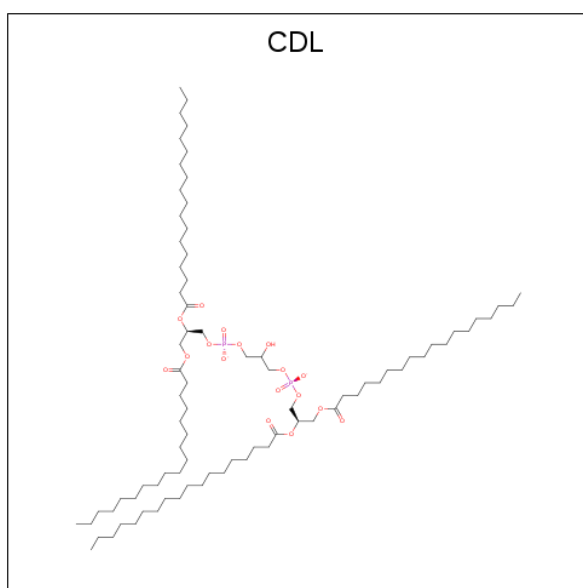
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	M	1	Total	Cl	0	0
			1	1		

- Molecule 9 is BACTERIOPHEOPHYTIN A (three-letter code: BPH) (formula: C₅₅H₇₆N₄O₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	M	1	Total	C	N	O	0	0
			65	55	4	6		
9	M	1	Total	C	N	O	0	0
			65	55	4	6		

- Molecule 10 is CARDIOLIPIN (three-letter code: CDL) (formula: $C_{81}H_{156}O_{17}P_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	M	1	Total	O	P	0	0
			10	8	2		

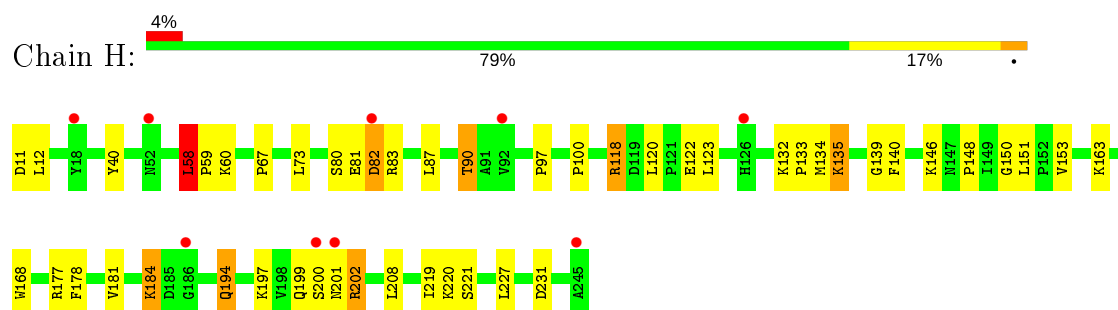
- Molecule 11 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	H	64	Total 64	O 64	0	0
11	L	43	Total 43	O 43	0	0
11	M	48	Total 48	O 48	0	0

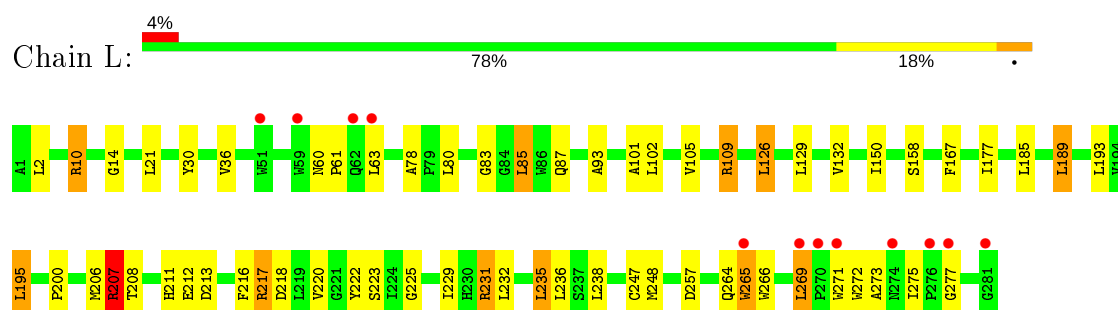
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($\text{RSRZ} > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

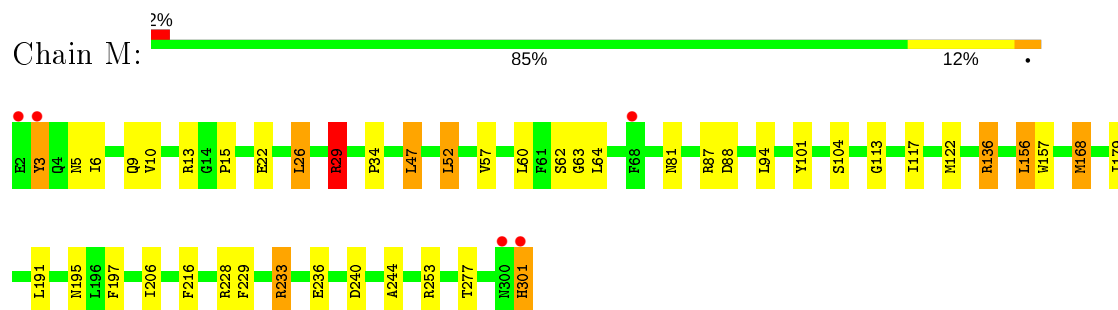
- Molecule 1: Reaction center protein H chain



- Molecule 2: Reaction center protein L chain



- Molecule 3: Reaction center protein M chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 4 ₂ 2 ₁ 2	Depositor
Cell constants a, b, c, α , β , γ	100.42Å 100.42Å 235.41Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.80 – 2.20 19.80 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.6 (19.80-2.20) 99.6 (19.80-2.20)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.04 (at 2.19Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.200 , 0.246 0.201 , 0.245	Depositor DCC
R_{free} test set	3129 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	24.2	Xtriage
Anisotropy	0.025	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.43 , 62.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7045	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.27% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BCL, LDA, CL, CDL, BPH, FE2, U10

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	H	0.92	2/1834 (0.1%)	0.89	5/2497 (0.2%)
2	L	0.92	1/2320 (0.0%)	0.98	13/3175 (0.4%)
3	M	0.91	0/2492	0.92	10/3401 (0.3%)
All	All	0.91	3/6646 (0.0%)	0.94	28/9073 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	H	0	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	L	30	TYR	CD1-CE1	-5.93	1.30	1.39
1	H	132	LYS	CE-NZ	5.41	1.62	1.49
1	H	132	LYS	CD-CE	5.15	1.64	1.51

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L	207	ARG	NE-CZ-NH2	-14.31	113.14	120.30
3	M	136	ARG	NE-CZ-NH2	-12.97	113.81	120.30
3	M	136	ARG	NE-CZ-NH1	11.77	126.19	120.30
2	L	217	ARG	NE-CZ-NH1	10.68	125.64	120.30
3	M	253	ARG	NE-CZ-NH2	-10.07	115.26	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	H	80	SER	Peptide

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	H	1787	0	1785	42	0
2	L	2232	0	2187	47	0
3	M	2400	0	2310	43	0
4	H	14	0	24	3	0
5	L	132	0	147	12	0
5	M	114	0	111	13	0
6	L	24	0	25	14	0
6	M	45	0	59	3	0
7	M	1	0	0	0	0
8	M	1	0	0	0	0
9	M	130	0	152	17	0
10	M	10	0	0	0	0
11	H	64	0	0	3	0
11	L	43	0	0	3	0
11	M	48	0	0	1	0
All	All	7045	0	6800	142	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 10.

The worst 5 of 142 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:L:1306:U10:H4M3	6:L:1306:U10:O3	1.42	1.14
1:H:118:ARG:HD3	1:H:120:LEU:HD12	1.28	1.13
2:L:206:MET:O	11:L:1348:HOH:O	1.69	1.08
6:L:1306:U10:C4M	6:L:1306:U10:O3	2.14	0.95
1:H:90:THR:HB	1:H:97:PRO:O	1.65	0.95

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	H	233/235 (99%)	225 (97%)	8 (3%)	0	100	100
2	L	279/281 (99%)	265 (95%)	13 (5%)	1 (0%)	34	37
3	M	298/300 (99%)	288 (97%)	10 (3%)	0	100	100
All	All	810/816 (99%)	778 (96%)	31 (4%)	1 (0%)	51	60

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	L	265	TRP

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	H	190/190 (100%)	176 (93%)	14 (7%)	13	14
2	L	220/220 (100%)	198 (90%)	22 (10%)	7	7
3	M	236/236 (100%)	220 (93%)	16 (7%)	16	17
All	All	646/646 (100%)	594 (92%)	52 (8%)	12	12

5 of 52 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	L	158	SER
2	L	220	VAL

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Mol	Chain	Res	Type
3	M	191	LEU
2	L	167	PHE
2	L	195	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
2	L	258	GLN
3	M	301	HIS
3	M	9	GLN
2	L	87	GLN
3	M	195	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 2 are monoatomic - leaving 10 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
6	U10	M	1305	-	45,45,63	2.57	11 (24%)	54,57,79	1.90	16 (29%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	BCL	L	1283	2	58,74,74	1.84	9 (15%)	69,115,115	2.22	27 (39%)
10	CDL	M	1309	-	8,8,99	1.77	3 (37%)	12,12,111	1.50	3 (25%)
6	U10	L	1306	-	24,24,63	2.55	7 (29%)	29,32,79	2.70	14 (48%)
5	BCL	M	1302	3	40,56,74	1.77	8 (20%)	47,93,115	2.42	17 (36%)
9	BPH	M	1284	-	64,70,70	1.87	10 (15%)	76,101,101	1.46	18 (23%)
5	BCL	M	1303	3	58,74,74	1.54	5 (8%)	69,115,115	2.31	24 (34%)
5	BCL	L	1282	2	58,74,74	1.32	7 (12%)	69,115,115	2.14	22 (31%)
9	BPH	M	1304	-	64,70,70	1.92	10 (15%)	76,101,101	1.67	17 (22%)
4	LDA	H	1310	-	10,13,15	2.11	1 (10%)	12,15,17	0.64	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	U10	M	1305	-	-	10/42/66/87	0/1/1/1
9	BPH	M	1304	-	1/1/18/22	21/54/105/105	0/5/6/6
6	U10	L	1306	-	-	6/17/41/87	0/1/1/1
5	BCL	M	1302	3	-	2/16/116/137	-
9	BPH	M	1284	-	1/1/18/22	11/54/105/105	0/5/6/6
5	BCL	M	1303	3	2/2/21/25	6/37/137/137	-
5	BCL	L	1282	2	2/2/21/25	15/37/137/137	-
5	BCL	L	1283	2	2/2/21/25	10/37/137/137	-
4	LDA	H	1310	-	-	4/11/11/13	-

The worst 5 of 71 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	M	1305	U10	C28-C29	6.88	1.49	1.33
5	M	1303	BCL	MG-NA	6.86	2.22	2.06
4	H	1310	LDA	O1-N1	-6.54	1.26	1.42
6	M	1305	U10	C33-C34	6.52	1.48	1.33
5	L	1283	BCL	MG-NC	-6.21	1.91	2.06

The worst 5 of 158 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	L	1282	BCL	CMB-C2B-C1B	-6.82	117.98	128.46
5	L	1283	BCL	CMB-C2B-C1B	-6.57	118.36	128.46
5	M	1302	BCL	CMB-C2B-C1B	-6.35	118.71	128.46
5	L	1282	BCL	CMB-C2B-C3B	6.17	136.23	124.68
5	L	1282	BCL	CAC-C3C-C4C	-6.14	98.97	112.58

5 of 8 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
9	M	1284	BPH	C8
5	M	1303	BCL	C8
5	M	1303	BCL	C13
5	L	1282	BCL	C8
5	L	1282	BCL	C13

5 of 85 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	M	1305	U10	C32-C33-C34-C35
6	M	1305	U10	C32-C33-C34-C36
6	M	1305	U10	C34-C36-C37-C38
6	L	1306	U10	C7-C8-C9-C10
6	L	1306	U10	C7-C8-C9-C11

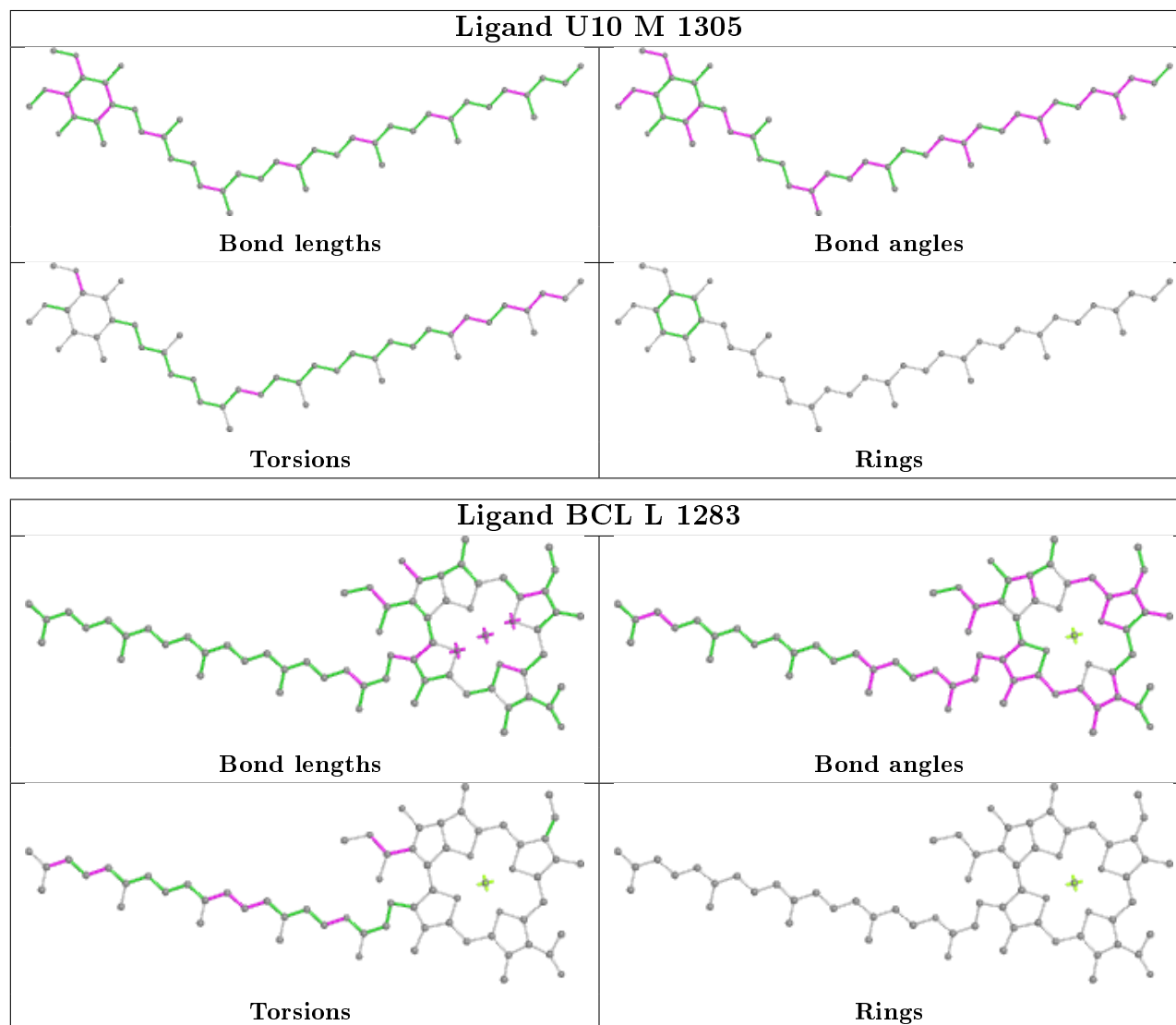
There are no ring outliers.

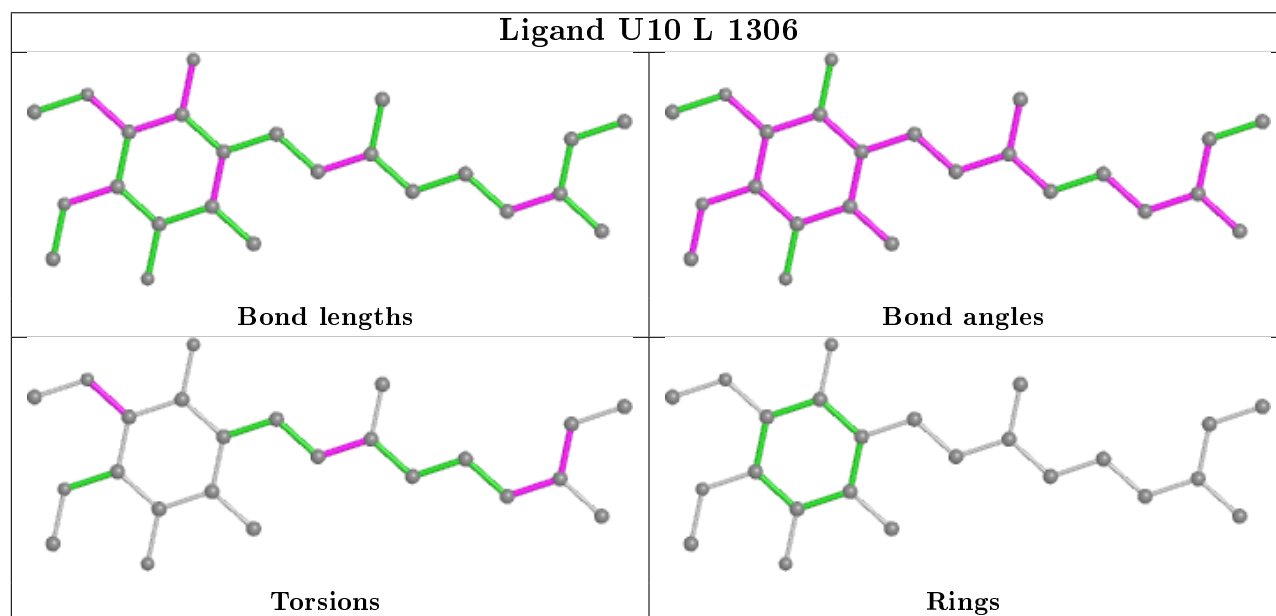
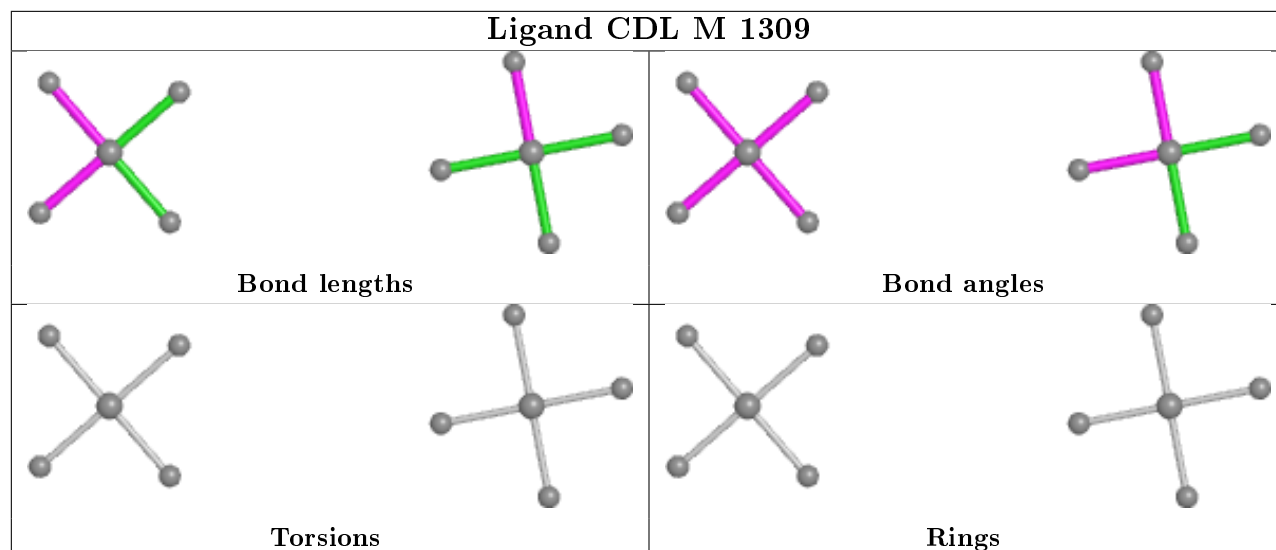
9 monomers are involved in 58 short contacts:

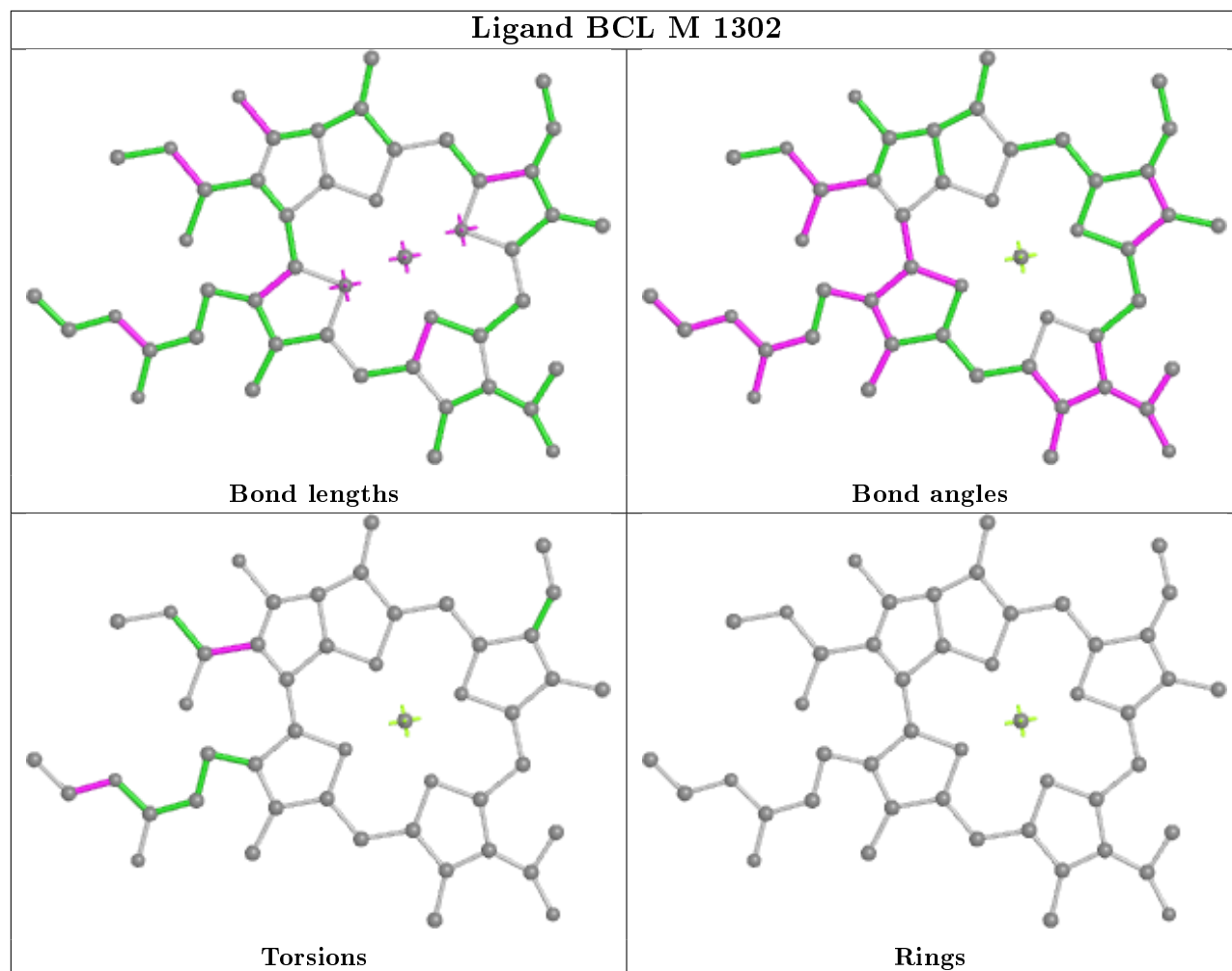
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	M	1305	U10	3	0
5	L	1283	BCL	5	0
6	L	1306	U10	14	0
5	M	1302	BCL	3	0
9	M	1284	BPH	5	0
5	M	1303	BCL	10	0
5	L	1282	BCL	8	0
9	M	1304	BPH	12	0
4	H	1310	LDA	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier.

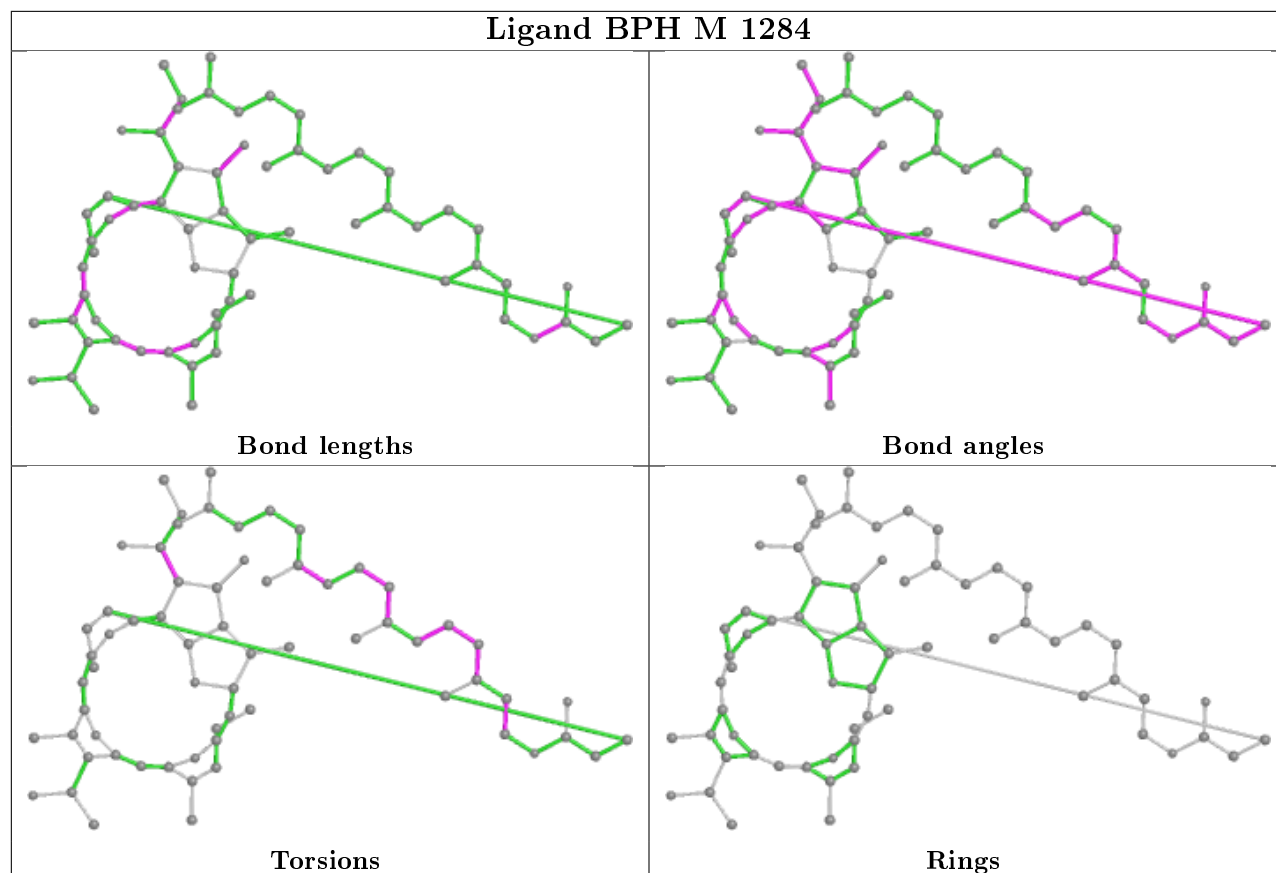
Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



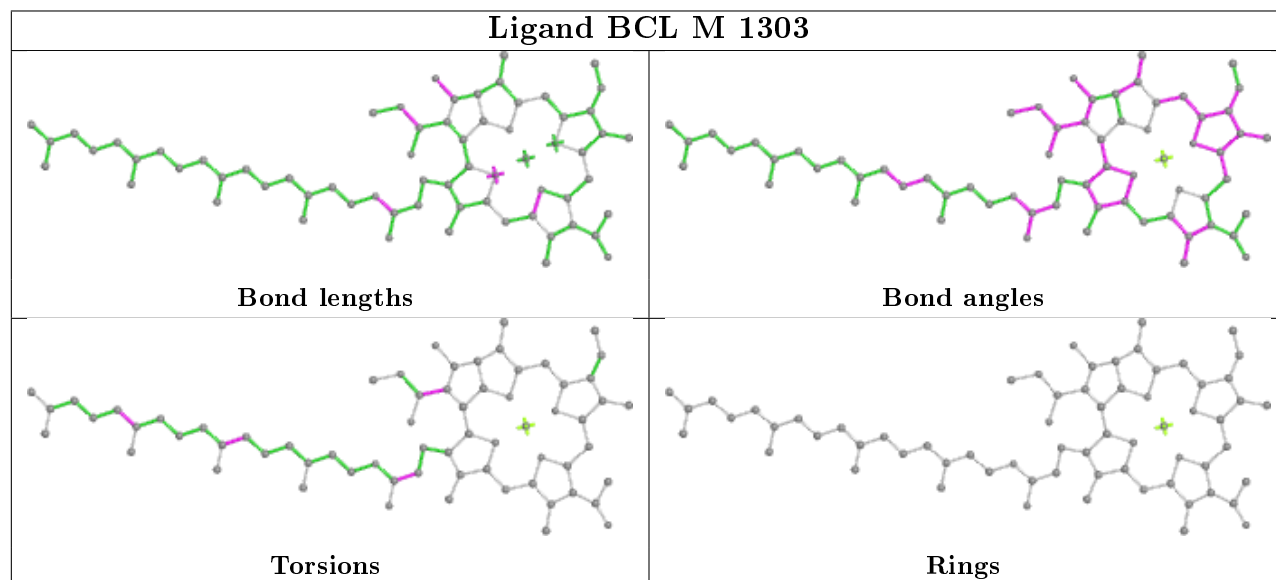


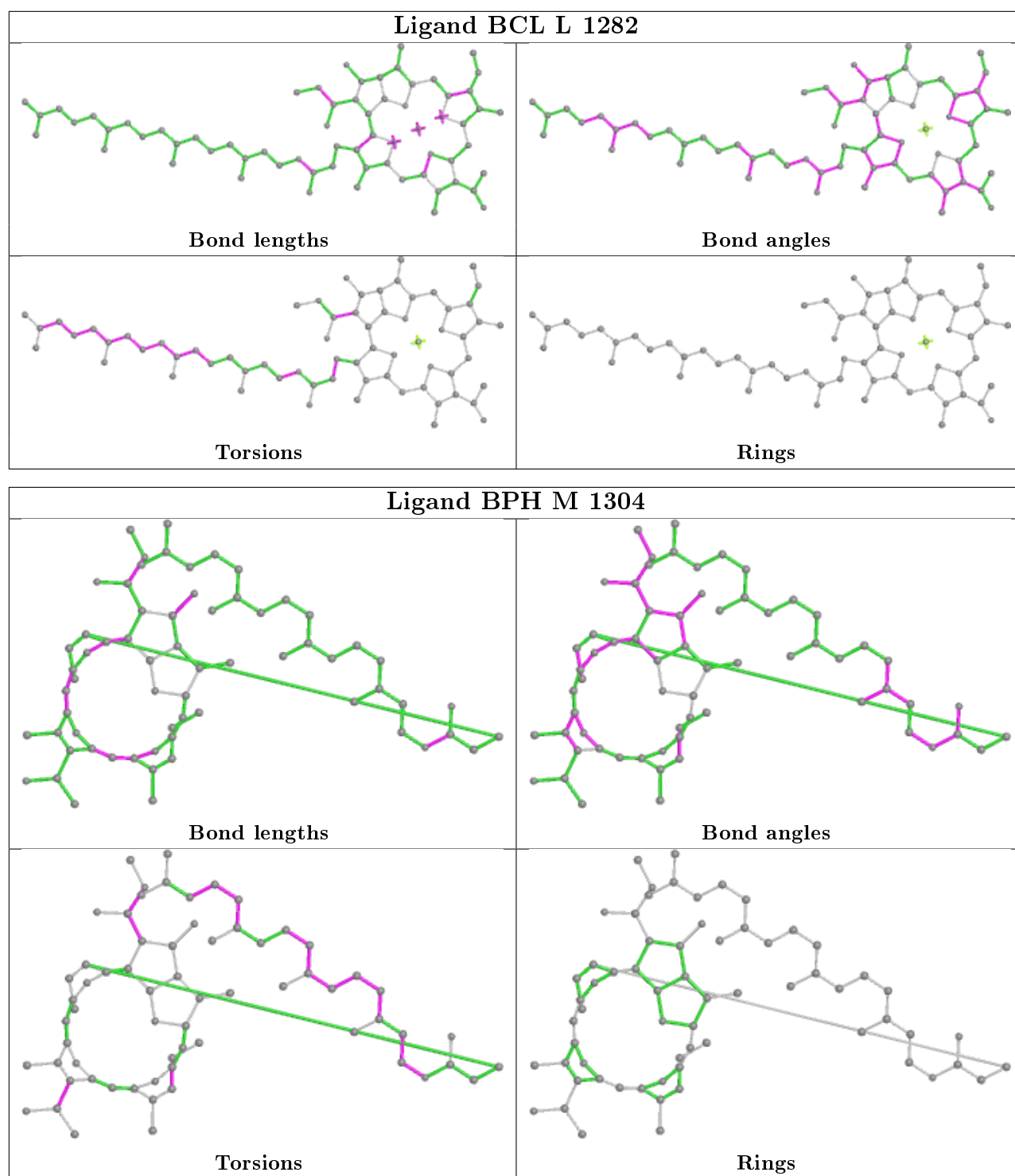


Ligand BPH M 1284



Ligand BCL M 1303





5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	H	235/235 (100%)	-0.20	9 (3%) 40 38	13, 28, 45, 50	0
2	L	281/281 (100%)	-0.30	12 (4%) 35 33	9, 24, 59, 65	0
3	M	300/300 (100%)	-0.51	5 (1%) 70 68	9, 23, 46, 68	0
All	All	816/816 (100%)	-0.35	26 (3%) 47 45	9, 25, 47, 68	0

The worst 5 of 26 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	L	281	GLY	6.6
2	L	59	TRP	5.9
3	M	301	HIS	5.6
2	L	276	PRO	5.0
3	M	300	ASN	4.4

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

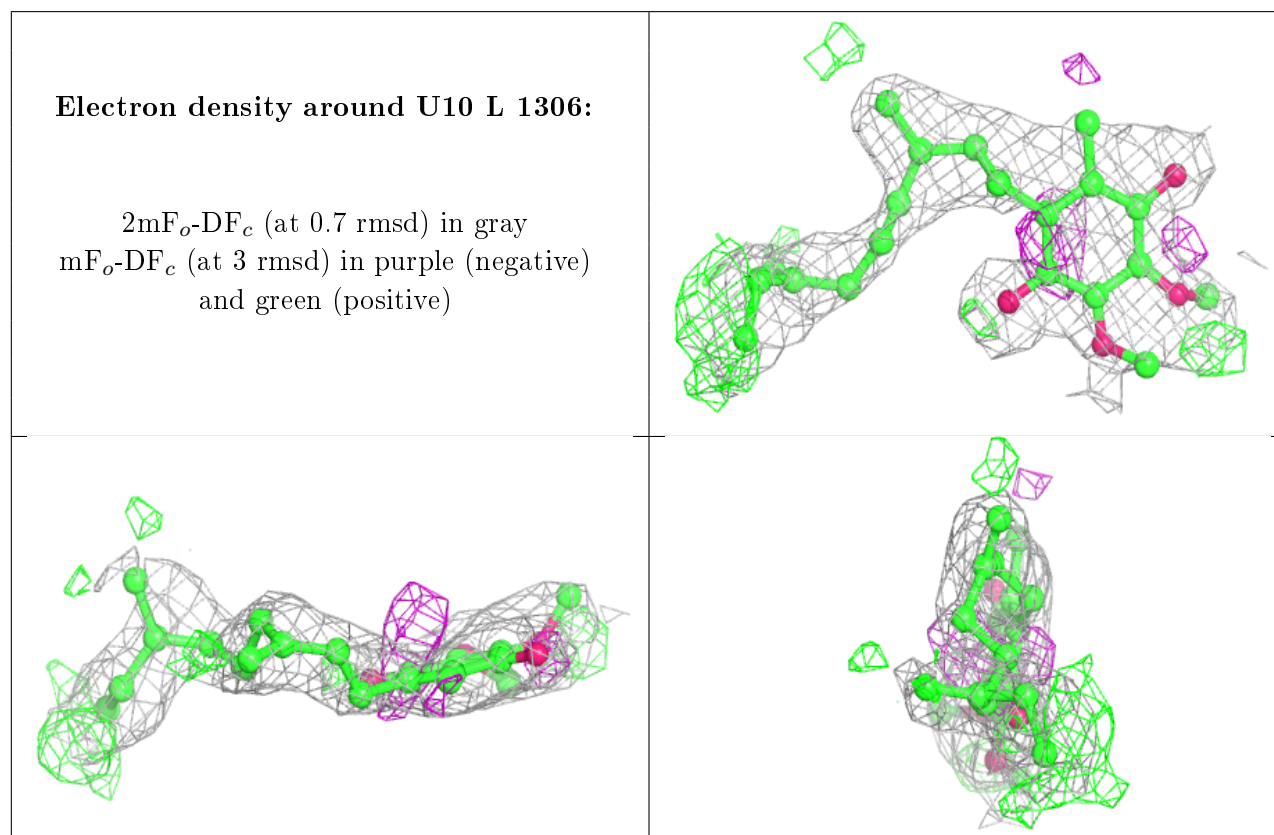
There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

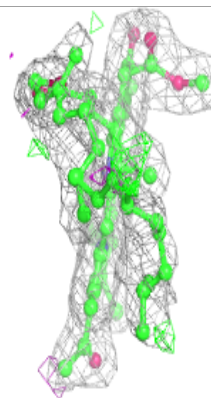
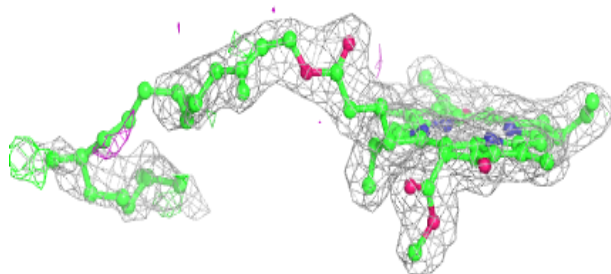
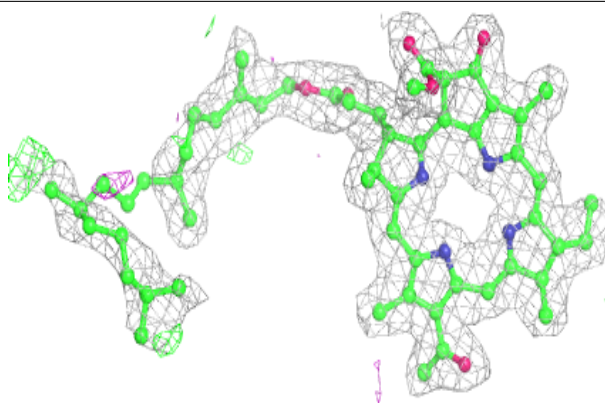
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
6	U10	L	1306	24/63	0.75	0.21	46,49,55,56	0
4	LDA	H	1310	14/16	0.89	0.12	30,38,42,45	0
9	BPH	M	1304	65/65	0.91	0.14	11,19,73,74	0
5	BCL	L	1282	66/66	0.92	0.14	15,22,28,37	0
5	BCL	M	1303	66/66	0.93	0.13	11,19,38,43	0
6	U10	M	1305	45/63	0.93	0.11	14,25,46,48	0
5	BCL	M	1302	48/66	0.94	0.09	14,19,27,29	0
5	BCL	L	1283	66/66	0.95	0.09	17,19,32,41	0
9	BPH	M	1284	65/65	0.96	0.10	9,15,31,33	0
8	CL	M	1308	1/1	0.98	0.05	38,38,38,38	0
10	CDL	M	1309	10/100	0.98	0.12	15,27,34,36	0
7	FE2	M	1307	1/1	1.00	0.05	14,14,14,14	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

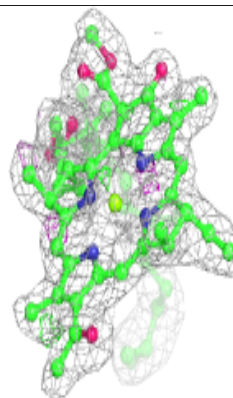
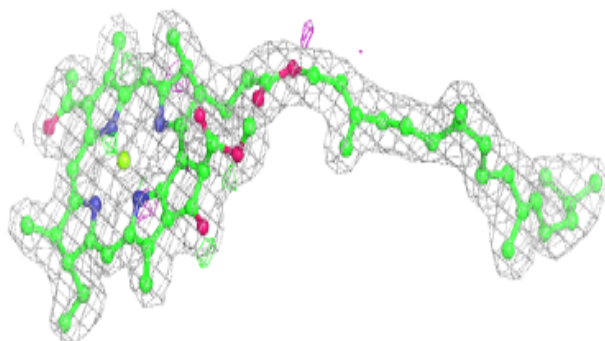
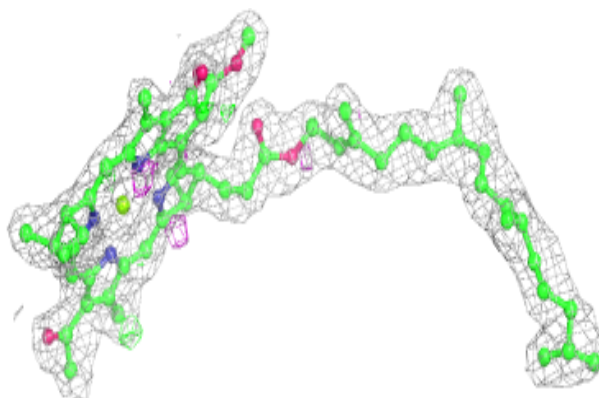


Electron density around BPH M 1304:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

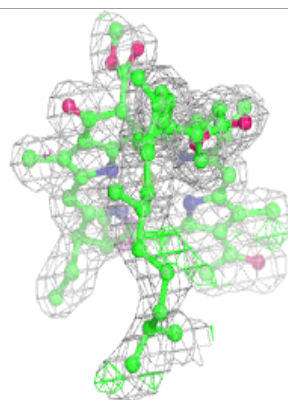
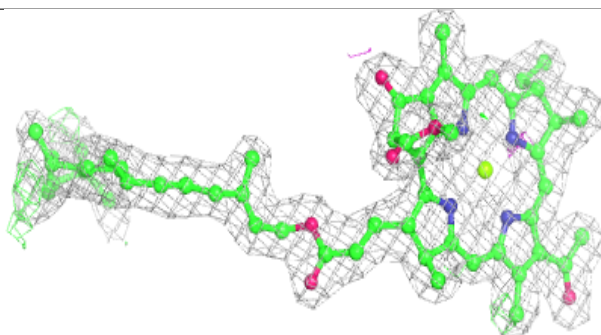
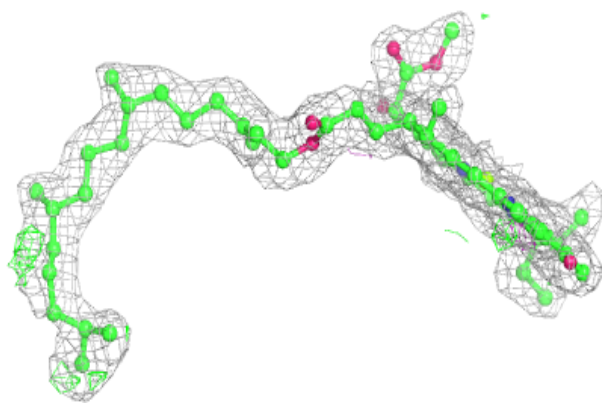
**Electron density around BCL L 1282:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

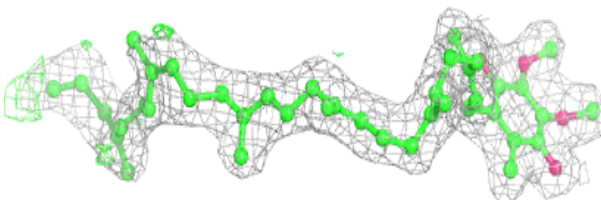
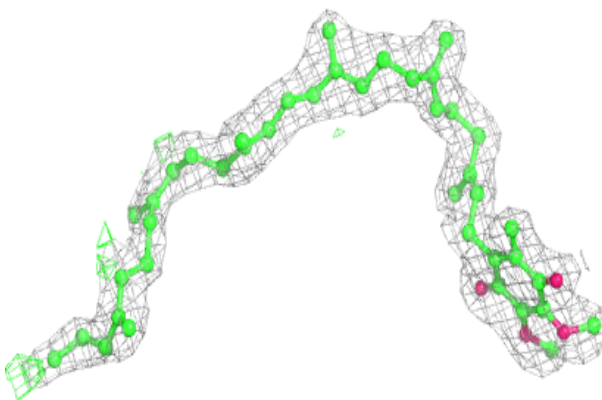


Electron density around BCL M 1303:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

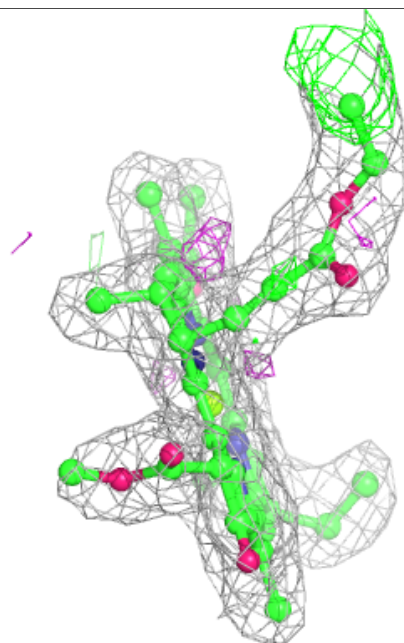
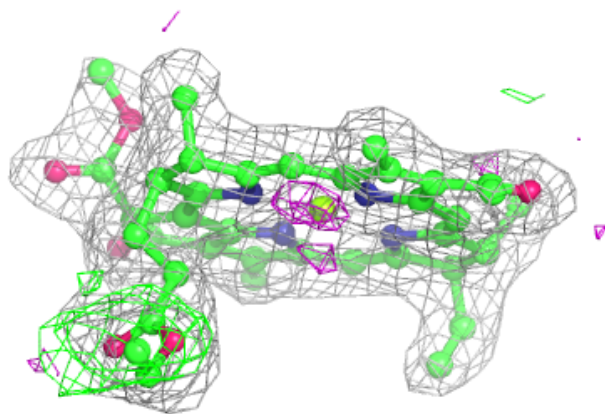
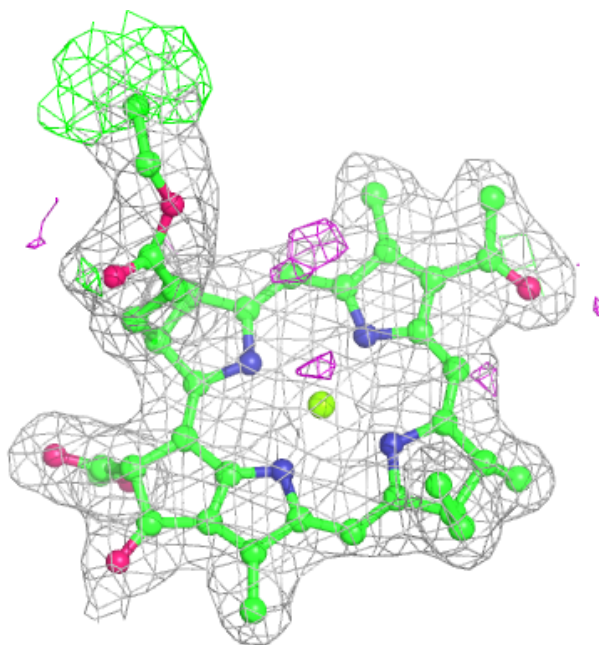
**Electron density around U10 M 1305:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



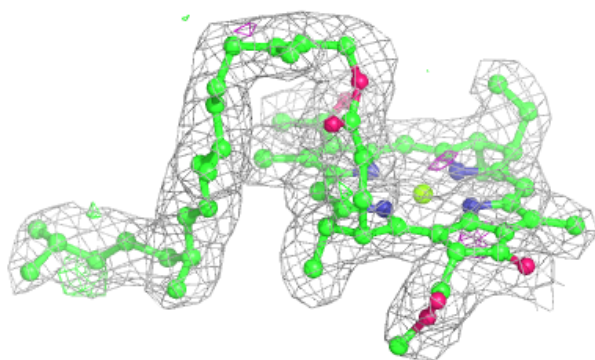
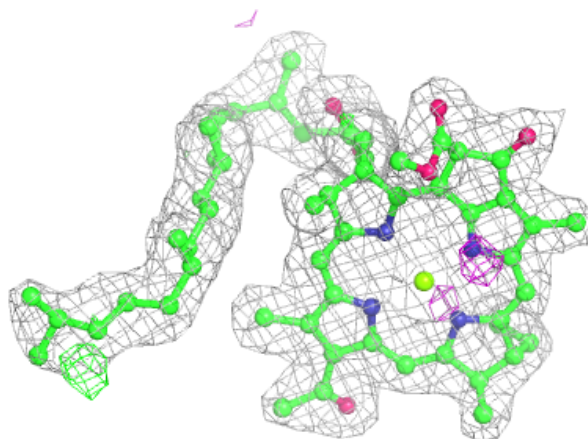
Electron density around BCL M 1302:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



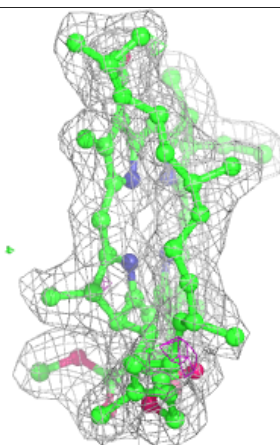
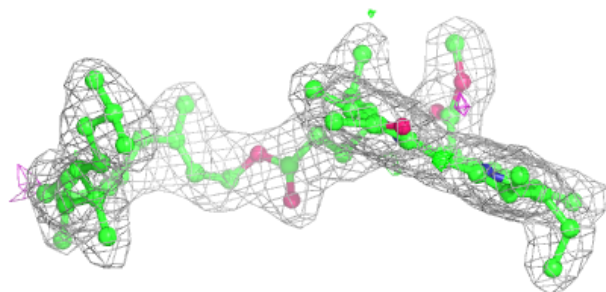
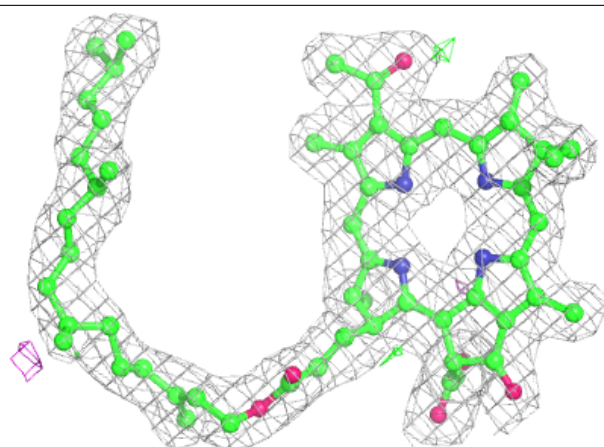
Electron density around BCL L 1283:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

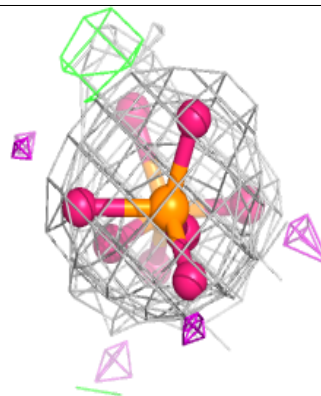
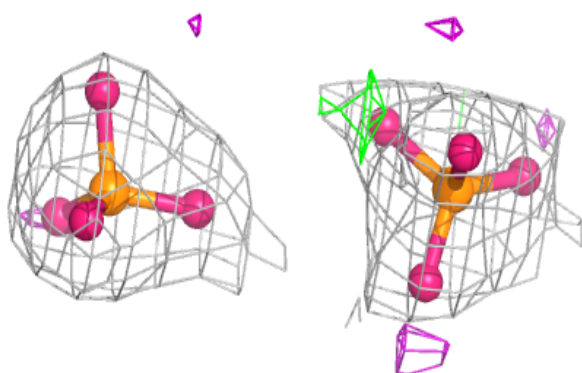
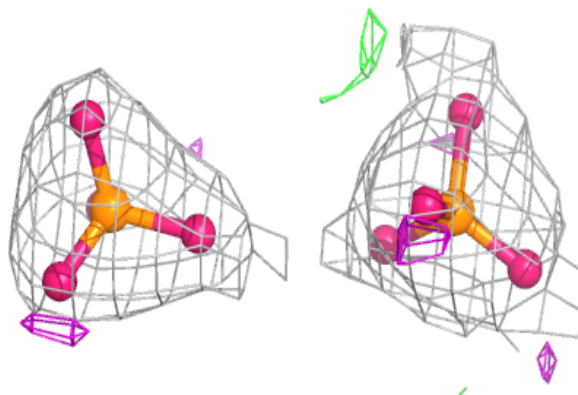


Electron density around BPH M 1284:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around CDL M 1309:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.